


```

Db      85 QFGQEPGSGNEIOVFACRFAEYFVFSKVNVNGKADPLKFKLSKGFGLSDIKWN 144
QY      144 FMKYLVPDCKVYVGMPTVSVSEVRLQITAVLRKLI 180
Db      145 FTKFLVDRGKVVDRVAPTTSS---PLSTIEKDKIKLL 177

RESULT  2
GSHY_ARATH STANDARD: PRT: 242 AA.
ID      GSHY_ARATH STANDARD: PRT: 242 AA.
AC      P52032.
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      01-MAR-2002 (Rel. 41, Last annotation update)
DE      Glutathione peroxidase homolog, chloroplast precursor (EC 1.11.1.9).
OS      Arabidopsis thaliana (Mouse-ear cress).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Eumetazoa; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX      NCBI_TaxID=3702;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=CV. COLUMBIA;
RA      Gachotte D., Benveniste P.;
RT      Cloning and sequencing of a glutathione peroxidase homologue from
RT      Arabidopsis thaliana.
RL      (In) Plant Gene Register PGR95-133.
CC      -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) -> oxidized
CC      glutathione + 2 H(2)O.
CC      -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
CC      -----
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CC      or send an email to license@sdb-sib.ch).
CC      -----
DR      EMBL; X89866; CAAG1965.1; -.
DR      HSSP; P00435; IGPI.
DR      InterPro: IPR000889; Glut_peroxidase.
DR      Pfam; PF00255; GSHPX; 1.
DR      PRINTS; PR01011; GLUTPROXOXASE.
DR      PROSITE; PS00460; GLUTATHIONE_PEROXID_1; 1.
DR      PROSITE; PS00763; GLUTATHIONE_PEROXID_2; 1.
KW      Peroxidase; Oxidoreductase; Transil peptide; Chloroplast.
FT      TRANSIT 1 64 CHLOROPLAST (POTENTIAL).
FT      CHAIN 65 242 GLUTATHIONE PEROXIDASE HOMOLOG.
FT      ACT_SITE 111 111 BY SIMILARITY.
SQ      SEQUENCE 242 AA; 26814 MW; 3A7031CCB416B57 CRC64;

Query Match 34.1%; Score 335; DB 1; Length 242;
Best Local Similarity 41.2%; Pred. No. 2.7e-25;
Matches 70; Conservative 24; Mismatches 66; Indels 10; Gaps 2;

QY      17 ACAQOEDYDFDKAVNIRKLVSLKRYGVSLLVNVNASEGCFDDHYRALQDLORDLGP 76
Db      71 ARRAAKRYVHDFYKIDKDALNFKGVMLIVNVAASGILSSNLSLHYEKYK 130
QY      77 HHENVLAPPCNOFGQEPDSNKEIESFACRTYSVSFPMRSKIAVGTGAHPAFKYLAAQTS 136
Db      131 OGFEILAFPCNOFGQEPDSNKEIKQFACRFAEPPFDKVDVNGPSTAPIVEFLKSNA 190
QY      137 G-----KEPTWFMKYLVPDCKVYVGMPTVSVSEVRLQITAVLRKLI 179
Db      191 GGFGLGILK---WNEKFLIDKKGVKVERYPPTSPFQIEKDIQKLLAEL 237

RESULT  3
GPO_SYNY3 STANDARD: PRT: 169 AA.
ID      GPO_SYNY3 STANDARD: PRT: 169 AA.

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AC      P74250;
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Putative glutathione peroxidase (EC 1.11.1.9).
GN      SLR1171.
OS      Synechocystis sp. (strain PCC 6803).
OC      Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX      NCBI_TaxID=1148;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE-97061201; PubMed-8905231;
RA      Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA      Miyajima N., Hiroseawa M., Sugiyama M., Sasamoto S., Kimura T.,
RA      Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA      Shimpou S., Takeuchi C., Wada T., Matsubae A., Yamada M., Yasuda M.,
RA      Tabata S.;
RT      "Sequence analysis of the genome of the unicellular cyanobacterium
RT      Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT      entire genome and assignment of potential protein-coding regions.";
RL      DNA Res. 3:109-136(1996).
CC      -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) -> oxidized
CC      glutathione + 2 H(2)O.
CC      -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
CC      -----
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CC      or send an email to license@sdb-sib.ch).
CC      -----
DR      EMBL; D90913; BAA18344.1; -.
DR      HSSP; P00435; IGPI.
DR      InterPro: IPR000889; Glut_peroxidase.
DR      Pfam; PF00255; GSHPX; 1.
DR      PRINTS; PR01011; GLUTPROXOXASE.
DR      PROSITE; PS00460; GLUTATHIONE_PEROXID_1; 1.
DR      PROSITE; PS00763; GLUTATHIONE_PEROXID_2; 1.
KW      Peroxidase; Oxidoreductase; Complete proteome.
FT      ACT_SITE 41 41 BY SIMILARITY.
SQ      SEQUENCE 169 AA; 18452 MW; 0DC382089CE39E2 CRC64;

Query Match 33.5%; Score 329.5; DB 1; Length 169;
Best Local Similarity 41.7%; Pred. No. 6.1e-25;
Matches 70; Conservative 20; Mismatches 67; Indels 11; Gaps 2;

QY      19 AQOEDYDFDKAVNIRKLVSLKRYGVSLLVNVNASEGCFDDHYRALQDLORDLGP 78
Db      3 AQANNTLYGFSANALDGSVALRDPEFGKYLIVNTASQCGFTPO-YQGLQALTNRFGRD 61
QY      79 FNVLAFFPCNOFGQEPDSNKEIESFACRTYSVSFPMRSKIAVGTGAHPAFKYLAAQTS 136
Db      62 FTVLGFPCNOFGQEPDSNKEIKFCETRGVTFLEKRVNGPNAHPFKYLTAAAPG 121
QY      137 -----GKEPTWFMKYLVPDCKVYVGMPTVSVSEVRLQITAVLRKLI 176
Db      122 MATPLFGAEDIKWNTKFLVDROGKVVKRYGSIAPDEIAIDIEKLL 169

RESULT  4
GSHC_SCHMA STANDARD: PRT: 169 AA.
ID      GSHC_SCHMA STANDARD: PRT: 169 AA.
AC      000277;
DT      01-DEC-1992 (Rel. 24, Created)
DT      01-DEC-1992 (Rel. 24, Last sequence update)
DT      01-MAR-2002 (Rel. 41, Last annotation update)
DE      Glutathione peroxidase (EC 1.11.1.9) (GPX).
GN      GPX1.
OS      Schistosoma mansoni (Blood fluke).
OC      Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminthes;

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OC Rhadithophora; Eulectrophora; Revertospermatia; Mediofusata;
 OC Neodermatia; Trematoda; Digenea; Strigeidae; Schistosomatidae;
 OC Schistosomatidae; Schistosoma.
 OX NCBI_TaxID=6183;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PUERTO RICAN;
 RX MEDLINE=92326859; PubMed=1625700;
 RA Williams D.L., Pierce R.J., Capron A.;
 RT "Molecular cloning and sequencing of glutathione peroxidase from
 Schistosoma mansoni";
 RL Mol. Biochem. Parasitol. 52:127-130(1992).
 RN [2]
 RP REVISION TO 43.
 RA Williams D.L., Pierce R.J., Capron A.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBD databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NMRL;
 RX MEDLINE=95203415; PubMed=7895842;
 RA Mel H., Loverde P.T.;
 RT "Schistosoma mansoni: cloning the gene encoding glutathione
 peroxidase";
 RL Exp. Parasitol. 80:319-322(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PUERTO RICAN;
 RX MEDLINE=94471027; PubMed=8125294;
 RA Roche C., Williams D.L., Khalife J., Lepreste T., Capron A.,
 Pierce R.J.;
 RT "Cloning and characterization of the gene encoding Schistosoma
 mansoni glutathione peroxidase";
 RL Gene 138:149-152(1994).
 CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized
 glutathione + 2 H(2)O.
 CC -1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS
 ENCODED BY THE OPAL CODON, UGA.
 CC -1- INDUCTION: GPX ACTIVITY INCREASES SIGNIFICANTLY AS WORMS MATURE IN
 THEIR HOST AND IS POSITIVELY CORRELATED TO THE RESISTANCE TO
 ANTIOXIDANTS.
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: M86510; AAA29885.2; ALT. SEQ.
 DR EMBL: L37762; AAC14468.2; ALT. SEQ.
 DR EMBL: L14329; AAB08485.2; ALT. SEQ.
 DR EMBL: L14328; AAB08485.2; JOINED.
 DR HSSP: P00435; IGPI.
 DR InterPro: IPR000889; Glut_peroxidase.
 DR Pfam: PF00255; GSHPx. 1.
 DR PRINTS: PR01011; GLUTPROXDAE.
 DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.
 DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
 KW Oxidoreductase; Peroxidase; Selenium; Selenocysteine.
 FT SE. CYS 43 43
 SO SEQUENCE 169 AA; 19424 MW; 55D877888F9FC10 CRC64;

Query Match 32.5%; Score 319; DB 1; Length 169;
 Best Local Similarity 43.9%; Pred. No. 6.3e-24;
 Matches 69; Conservative 21; Mismatches 63; Indels 4; Gaps 1;

QY 26 YDFKAVNIGKLVSLKRGYSVSLVNVASGCGFTDQHRALDQORDGPHFNLAP 85
 DB 12 YETVDINGVDVSLKRGYHCVLLIVNACGCGATDKRNYRLOEDMHTLVGKGLRILAP 71

OY 86 CNOFGOEPPDSNKEISFACRTYSVFPMSKIAVGTGHAHPKYLIAO----TSGKEPT 141
 DB 72 CNOFGOEPPMAEIKFTYERKGVQFDMFSKIKVNSDADDLKRLKSNQHTLNNIK 131
 OY 142 WNFMYLVAADGKVVAGAMPFTVSVEEVRILQITALVKK 178
 DB 132 WNFSEFLVDROGQPVKRYSPPTAPYDIEGIMWELKK 168
 RESULT 5
 ID GSX2_CITSI STANDARD; PRT; 167 AA.
 AC 006652;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Glutathione peroxidase homolog (Ec 1.11.1.9) (Salt-associated
 protein).
 DE CSA.
 GN Citrus sinensis (Sweet orange).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Sapindales; Rutaceae; Citrus.
 OX NCBI_TaxID=7111;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=93222490; PubMed=8467085;
 RA Holland D., Ben-Hayyim G., Falcin Z., Camoin L., Strosberg A.D.,
 Eshdat Y.;
 RT "Molecular characterization of salt-stress-associated protein in
 citrus: protein and cDNA sequence homology to mammalian glutathione
 peroxidases";
 RL Plant Mol. Biol. 21:923-927(1993).
 CC -1- FUNCTION: MAY CONSTITUTE A GLUTATHIONINE PEROXIDASE-LIKE
 PROTECTIVE SYSTEM AGAINST OXIDATIVE STRESSES.
 CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized
 glutathione + 2 H(2)O.
 CC -1- INDUCTION: BY SALT STRESS.
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: X66377; CAA47018.1; -
 DR HSSP: P00435; IGPI.
 DR InterPro: IPR000889; Glut_peroxidase.
 DR Pfam: PF00255; GSHPx. 1.
 DR PRINTS: PR01011; GLUTPROXDAE.
 DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.
 DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
 KW Oxidoreductase; Peroxidase.
 FT ACT_SITE 41 41
 SO SEQUENCE 167 AA; 18596 MW; DB6BDDC363F3260 CRC64;

Query Match 32.3%; Score 318; DB 1; Length 167;
 Best Local Similarity 39.2%; Pred. No. 7.8e-24;
 Matches 65; Conservative 28; Mismatches 65; Indels 8; Gaps 2;

QY 19 AQQEODFYDFKAVNIGKLVSLKRGYSVSLVNVASGCGFTDQHRALDQORDGPHN 78
 DB 3 SOKSTSVHDFTVADAKGQVDLSITKGLLIVNVAQCGLTNSNTELSQLYDKVKNKG 62
 QY 79 FNVLAFFCNOFGOEPPDSNKEISFACRTYSVFPMSKIAVGTGHAHPKYLIAO-- 136
 DB 63 LELIAFFCNOFGOEPPDSNKEISFACRTYSVFPMSKIAVGTGHAHPKYLIAO-- 122
 QY 137 --GKEPTWNFMYLVAADGKVVAGAMPFTVSVEEVRILQITALVKKLI 180

Db 123 LFGDSIKMNSKFLVDEKGNVVERIAPTTS-----PLSIEKDIRKLL 164

RESULT 6

GSNH_HUMAN STANDARD: PRT; 167 AA.

AC 023970;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Glutathione peroxidase 1 (EC 1.11.1.9).

GN GPXHA-1.

OS Helianthus annuus (Common sunflower).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;

OC Helianthaceae; Helianthus.

OX NCBI_TaxID=4232;

ON [1]

RP SEQUENCE FROM N.A.

RA Drevel J.R., Gagne G., Tourvieille de Labrouhe D., Nicolas P.,

RA Dufreue J.P., Ledolgt G., Roedel-Drevel P.;

RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: MAY CONSTITUTE A GLUTATHIONE PEROXIDASE-LIKE

CC PROTECTIVE SYSTEM AGAINST OXIDATIVE STRESSES.

CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized

CC glutathione + 2 H(2)O.

CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.

CC

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CC

CC EMBL: Y14429; CAA74775.1; -.

DR HSSP: P00435; IGPI.

DR InterPro: IPR000889; Glut_peroxidase.

DR Pfam: PF00255; GSHPx; 1.

DR PRINTS: PRO1011; GLUTPROXIDASE.

DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.

DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.

DR Oxidoreductase; Peroxidase.

KW ACT_SITE 41

FT ACET_SITE 41

SQ SEQUENCE 167 AA; 18842 MW; CFSAC7ACCT6558C9 CRC64;

Query Match 32.1%; Score 316; DB 1; Length 167;

Best Local Similarity 41.0%; Pred. No. 1.2e-23;

Matches 66; Conservative 23; Mismatches 68; Indels 4; Gaps 1;

OY 20 QOEDQFYDEKAVNRKGLVLEKRGVSLLVNVVASECGFTDOHYRALQOLQDLCPHHR 79

DB 4 QSKRTLYDFTVADAKGNDVLDLVYKGVLLVNVASKGGLTNSYDELNDQILYKKEKGF 63

OY 80 NVLAFCNFGQOEDPSNKEIESFACRTYSVSPMRSKTAVYTGTAHPFKYLAQ-----T 135

DB 64 ELIAFCNFGQOEDPSTNKEIYDFVCTKRSFPIDKVDNENAPAYEFLKTFPGYGI 123

OY 136 SCKEPTNFMKYLAVDPGKVGAMDPTVSVSEYRLQITLV 176

DB 124 LGGDIOMNFSKFLVDMKNGQVDCYPTTSLYVERDIQKLL 164

RESULT 7

GSNH_HUMAN STANDARD: PRT; 197 AA.

AC P36369; 043381.

DT 01-JUN-1994 (Rel. 29, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Phospholipid hydroperoxide glutathione peroxidase, mitochondrial

DE precursor (EC 1.11.1.9) (GPX4).

GN GPX4.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

ON [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Testis;

RX MEDLINE=94314239; PubMed=8039723;

RA Esworth R.S., Doan K., Doroshov J.H., Chu F.-F.;

RT "Cloning and sequencing of the cDNA encoding a human testis

RT phospholipid hydroperoxide glutathione peroxidase.";

RL Gene 144:317-318(1994).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=98381025; PubMed=9705830;

RA Keiner M.J., Montoya M.A.;

RT "Structural organization of the human selenium-dependent phospholipid

RT hydroperoxide glutathione peroxidase gene (GPX4): chromosomal

RT localization to 19p13.3.";

RL Biochem. Biophys. Res. Commun. 249:53-55(1998).

RN [3]

RP SEQUENCE FROM N.A.

RA Lamerdin J.E., McCreedy P.M., Skowronski E., Adamson A.W.,

RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S.,

RA Phan H., Velasco N., Ganes J., Dangnan L., Poundstone P.,

RA Christensen M., Georgescu A., Avila J., Liu S., Altix C., Andreise T.,

RA Trankelm M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,

RA Brice R., Thomas P., Quan G., Kronmiller B., Arellano A.,

RA Montgomerly M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,

RA Carraro A.V.;

RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: COULD PLAY A MAJOR ROLE IN PROTECTING MAMMALS FROM THE

CC TOXICITY OF INGESTED LIPID HYDROPEROXIDES

CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized

CC glutathione + 2 H(2)O.

CC -1- COPACITOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS

CC ENCODED BY THE OPAL CODON, UGA.

CC -1- SUBCELLULAR LOCATION: Mitochondrial and cytoplasmic.

CC -1- ALTERNATIVE PRODUCTS: A SINGLE NUCLEAR GENE PRODUCES BOTH FORMS

CC BY USE OF ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.

CC -1- TISSUE SPECIFICITY: PRESENT PRIMARILY IN TESTIS.

CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.

CC

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CC

CC EMBL: X71973; CAA50793.1; ALT-SEQ.

DR EMBL: AF060972; AAC32261.1; ALT-SEQ.

DR EMBL: AC004151; AAC03239.1; ALT-SEQ.

DR HSSP: P00435; IGPI.

DR MIM: 138322; -.

DR InterPro: IPR000889; Glut_peroxidase.

DR Pfam: PF00255; GSHPx; 1.

DR PRINTS: PRO1011; GLUTPROXIDASE.

DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.

DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.

DR Oxidoreductase; Peroxidase; Selenium; Selenocysteine;

KW Mitochondrion; Transit peptide; Alternative initiation.

KW Mitochondrion (POTENTIAL).

FT TRANSIT 1

FT CHAIN 2

FT CHAIN 197

FT CHAIN 28

FT CHAIN 197

FT INIT_MET 28

FT INIT_MET 28

FOR CYTOPLASMIC ISOFORM.

PEROXIDASE, MITOCHONDRIAL ISOFORM.

PHOSPHOLIPID HYDROPEROXIDE GLUTATHIONE

PEROXIDASE, CYTOPLASMIC ISOFORM.

FT SE.CYS 73 73
SQ SEQUENCE 197 AA: 22128 MW: 1AE3A2DAEC8FCB1 CRC64:

Query Match 31.6%: Score 311: DB 1: Length 197:

Best Local Similarity 43.9%: Pred. No. 4.5e-23:

Matches 68: Conservative 25: Mismatches 50: Indels 12: Gaps 4:

OY 18 CAQOE-----ODEYDEKAVNIRKGLVLEKRGSVSLVYVNSEGGFTPOHRAIQLOLR 72
DB 29 CASRDMRCARSMHESADIDGHMVLNDRKRGFCIVTNVNSQCGKTEVNTQILDHA 88
OY 73 DLGPHFNVLAPPCNFGQOEPDSNKEIESFACRTYSVSFPMFSKTAIVGTGAPAFKYL 132
DB 89 RFAEGGLRLAPPCNFGQOEPDSNKEIEKFAA-GYNVAFDMFSKICVNGDAHPLMKM 147
OY 133 -AQTSGK-----EPTWNEFKYLVAPDGKVVGAMP 161
DB 148 KIOPKKGILGNAIKWNFTFKLDKNGCYVRRYGP 182

RESULT 8

GSNH_NICSY STANDARD: PRT; 169 AA.

AC P30708;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Glutathione peroxidase homolog 6P229 (EC 1.11.1.9).
OS Nicotiana sylvestris (Wood tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots;
OC Asteridae: eusteridae I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4096;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=Protoplast;
RA MEDLINE=92163033; PubMed=1536938;
RA Criqui M.C., Jamet E., Parmentier Y., Marbach J., Durr A., Fleck J.;

RT "Isolation and characterization of a plant cDNA showing homology to
animal glutathione peroxidases.";

RL Plant Mol. Biol. 18:623-627(1992).

CC -1- FUNCTION: MAY CONSTITUTE A GLUTATHIONE PEROXIDASE-LIKE
PROTECTIVE SYSTEM AGAINST OXIDATIVE STRESSES.

CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized
glutathione + 2 H(2)O.

CC -1- TISSUE SPECIFICITY: GERMINATING SEED, ABEEX, FLOWER, AS WELL AS IN
STRESSED TISSUES.

CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.

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DR EMBL: X60219; CAA42780.1; -
DR PIR: S20501; S20501.
DR HSSP: P00435; IGPI.
DR InterPro: IPR000889; Glut_peroxidase.
DR Pfam: PF00255; GSHPx. 1.
DR PRINTS: PRO1011; GLUTPROXADSE.
DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.
DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
KW Oxidoreductase; Peroxidase.
FT ACT_SITE 43
FT SEQUENCE 169 AA: 18767 MW: 401913069E1E97C7 CRC64;

Query Match 31.4%: Score 309: DB 1: Length 169:
Best Local Similarity 36.4%: Pred. No. 5.9e-23:

Matches 60: Conservative 31: Mismatches 70: Indels 4: Gaps 1:

OY 16 AACAOEOEDFYDEKAVNIRKGLVLEKRGSVSLVYVNSEGGFTPOHRAIQLOLRD 75
DB 2 ASQSKPQSIYDFTYVDAGNDVLSIRKGLVILVNVASQGLNSNTDITLTIKKKK 61
OY 76 PHEFNVLAPPCNFGQOEPDSNKEIESFACRTYSVSFPMFSKTAIVGTGAPAFKYL 135
DB 62 DQLELTLAPPCNFGQOEPDSNKEIEIQNMCTRKAEYPIFDKYDVGNDNAAPLTKLKS 121
OY 136 S-----GKEPTWNEFKYLVAPDGKVVGAMPDYVSVEEVRQITLV 176
DB 122 KGFEGDSIKWNFSKFLVDKGNVVDYRSPYTPASMERDICKLL 166

RESULT 9

GSNH_MOUSE STANDARD: PRT; 197 AA.

AC 070325;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phospholipid hydroperoxide glutathione peroxidase, mitochondrial
precursor (EC 1.11.1.9) (PBGpx) (GPX-4).
GN GPX4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=FAH/B, AND C57BL/6J; TISSUE=Testis, and Myocardium;
RX MEDLINE=99272820; PubMed=10341094;

RA Knopp E.A., Arndt T.L., Eng K.L., Caldwell M., LeBeauf R.C.,
Deeb S.S., O'Brien K.D.;

RT "Murine phospholipid hydroperoxide glutathione peroxidase: cDNA
sequence, tissue expression, and mapping.";

RL Mamm. Genome 10:601-605(1999).

CC -1- FUNCTION: COULD PLAY A MAJOR ROLE IN PROTECTING MAMMALS FROM THE
TOXICITY OF INGESTED LIPID HYDROPEROXIDES.

CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized
glutathione + 2 H(2)O.

CC -1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS
ENCODED BY THE OPAL CODON, UGA.

CC -1- SUBCELLULAR LOCATION: Mitochondrial and cytoplasmic.
BY USE OF ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.

CC -1- TISSUE SPECIFICITY: PRESENT PRIMARILY IN TESTIS.

CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.

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or send an email to license@sib-sib.ch).

DR EMBL: AF045768; AAC18832.1; ALT_INT.
DR EMBL: AF045769; AAC18833.1; ALT_INT.
DR EMBL: AF044056; AAC14560.1; -
DR HSSP: P00435; IGPI.
DR MGD: MGI:104767; GPX4.
DR InterPro: IPR000889; Glut_peroxidase.
DR Pfam: PF00255; GSHPx. 1.
DR PRINTS: PRO1011; GLUTPROXADSE.
DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.
DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
KW Oxidoreductase; Peroxidase; Selenium; Selenocysteine;
KW Mitochondrion; Transit peptide; Alternative initiation.
FT TRANSIT 1
FT CHAIN ? 197
FT MITOCHONDRION (POTENTIAL).
FT PHOSPHOLIPID HYDROPEROXIDE GLUTATHIONE
FT PEROXIDASE, MITOCHONDRIAL ISOFORM.

RP CHARACTERIZATION.
RC TISSUE-Testis:
RX MEDLINE-92210587; PubMed-1556123;
RA Roveri A., Cassaso A., Maiorino M., Dalan P., Calligaro A., Ursini F.,
RT "Phospholipid hydroperoxide glutathione peroxidase of rat testis.
RT Gonadotropin dependence and immunocytochemical identification.",
RL J. Biol. Chem. 267:6142-6146(1992).
CC -I- FUNCTION: COULD PLAY A MAJOR ROLE IN PROTECTING MAMMALS FROM THE

US *Lactococcus lactis* (subsp. cremoris) (*Streptococcus cremoris*).
 OC Bacteria: Firmicutes, Bacillus/Clostridium group; Streptococcaceae.
 OC Lactococcus.
 OX NCBI_taxid=1359;
 RN [1]
 RP SEQUENCE FROM N.A.

CC STRAIN-MG1363;
 RA Martinussen J.;
 RT "The carb gene encoding the large subunit of carbamoylphosphate
 synthetase from *Lactococcus lactis* is monocistronic.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized
 glutathione + 2 H(2)O.
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
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 CC -----
 CC EMBL: AJ000109; CAA03927.1; -.
 DR HSSP: P00435; 1GPI.
 DR InterPro: IPR000889; Glut_peroxidase.
 DR Pfam: PF00255; GSHpx; 1.
 DR PRINTS: PR01011; GLUTPROXDAE.
 DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.
 DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
 KW Peroxidase; Oxidoreductase.
 FT ACT_SITE 35 35
 SQ SEQUENCE 157 AA; 17969 MW; AD6C53806E03C7E9 CRC64;

Query Match 31.1%; Score 305.5; DB 1; Length 157;
 Best Local Similarity 39.5%; Pred. No. 1.4e-22;
 Matches 62; Conservative 26; Mismatches 64; Indels 5; Gaps 2;
 Oy 24 DFDFKAVNRIGKLVSEKRGSVSLVNVASGFTDQHYRALQOLRDLPGRHFNVLTA 83
 Db 2 NTFDFSAVKMNGETVMSKDYKGVVYVNTASKGFTPO-FEGLEKLYETTKQGLEILG 60
 Oy 84 FPCNGGQEPDSNKEIESFACRTYSVSPMFESKIAVTGTGAHPARKYLAOTS-----GKE 139
 Db 61 FPCNGANDAGENTEINEFCQNLNGVTFTMFQKIKVNGEAMPLVQFLKKAAGKALSGT 120
 Oy 140 PTNPFMKYLVAPDGKVVGVGADPTVSVEVRLQITLALV 176
 Db 121 IKWNTFKFLIDRGQVIERPAPKTEPEMEETIKLL 157

RESULT 12
 BTUE_ECOLI STANDARD; PRT; 183 AA.
 AC P06610;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Vitamin B12 transport periplasmic protein btue.
 GN BTUE OR B1710.
 OS *Escherichia coli*.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC *Escherichia*.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=86304184; PubMed=3528129;
 RA Friedrich M.J., Devaux L.C., Kadner R.J.;
 RT "Nucleotide sequence of the btueC genes involved in vitamin B12
 RT transport in *Escherichia coli* and homology with components of
 RT periplasmic-binding-protein-dependent transport systems.";
 RL J. Bacteriol. 167:928-934(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN-K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 RL Science 277:1453-1474(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=97251357; PubMed=9097039;
 RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
 RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
 RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
 RA Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y.,
 RA Oshima T., Saito N., Sampaio G., Seki Y., Sivasubram S.,
 RA Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
 RA Yamamoto Y., Horuchi T.;
 RT "A 570-kb DNA sequence of the *Escherichia coli* K-12 genome
 RT corresponding to the 28.0-40.1 min region on the linkage map.";
 RL DNA Res. 3:363-377(1996).
 CC -1- FUNCTION: NOT ESSENTIAL FOR B12 TRANSPORT. HOWEVER, IT IS AN
 CC AUXILIARY COMPONENT OF THE TRANSPORT SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Periplasmic (Probable).
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: M14031; AAA23527.1; -.
 DR EMBL: AE000266; AAC74780.1; -.
 DR EMBL: D90813; BAA15478.1; -.
 DR EMBL: D90814; BAA15490.1; -.
 DR PIR: B24498; QRECBP.
 DR HSSP: P00435; 1GPI.
 DR EcoGene: EG10129; btue.
 DR InterPro: IPR000889; Glut_peroxidase.
 DR Pfam: PF00255; GSHpx; 1.
 DR PRINTS: PR01011; GLUTPROXDAE.
 DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.
 DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
 KW Periplasmic; Cobalt transport; Complete proteome.
 SQ SEQUENCE 183 AA; 20469 MW; C8DB671963A7F235 CRC64;

Query Match 31.1%; Score 305.5; DB 1; Length 183;
 Best Local Similarity 40.0%; Pred. No. 1.4e-22;
 Matches 64; Conservative 29; Mismatches 42; Indels 25; Gaps 3;
 Oy 32 NINGKLVSEKRGSVSLVNVASGFTDQHYRALQOLRDLPGRHFNVLAPPCNFGQ 91
 Db 12 DIDGEVTLTEKFAVNYLLIVNVASKGGLTPO-YEOLNENKQAWVDKGFVGLGFCNQFLE 70
 Oy 92 QEPDSNKEIESFACRTYSVSPMFESKIAVTGTGAHPARKYLAQ----- 134
 Db 71 QEPGSDPEITTCCTTNGVTFPPMFESKIEVNGEGRHPLXQXLAAPTAAPADESGFYARM 130
 Oy 135 -TSGKEP-----TNPFMKYLVAPDGKVVGVGADPTVSVEE 167
 Db 131 VSKGRAFLYDPDILIMNEFKFLVGRDKVIGRFSPDMTPED 170
 RESULT 13
 GSHH_PIG STANDARD; PRT; 197 AA.
 AC P36968;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Phospholipid hydroperoxide glutathione peroxidase, mitochondrial
 DE precursor (EC 1.1.1.9) (PhGPx) (GPX-4).

GN GPX4.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93312346; PubMed=8323565;
RA Sunde R.A., Dyer J.A., Moran T., Evenson J.K., Sugimoto M.;
RT "Phospholipid hydroperoxide glutathione peroxidase: full-length pig
RT blastocyst cDNA sequence and regulation by selenium status.";
RL Biochem. Biophys. Res. Commun. 193:905-911(1993).
RN [2]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC TISSUE=Liver, and Heart;
RX MEDLINE=9411752; PubMed=8125951;
RA Brigelius-Flohe R., Aumann K.-D., Bloecker H., Gross G.,
RA Klotzsch K.-D., Majorino M., Roveri A., Schuckelt R., Ursini F.,
RA Wiegand E., Flohe L.;
RT "Phospholipid-hydroperoxide glutathione peroxidase. Genomic DNA,
RT cDNA, and deduced amino acid sequence.";
RL J. Biol. Chem. 269:7342-7348(1994).
RN [3]
RP SEQUENCE OF 40-197 FROM N.A. AND PARTIAL SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=92137773; PubMed=1778506;
RA Schuckelt R., Brigelius-Flohe R., Majorino M., Roveri A., Reunkens J.,
RA Strassburger W., Ursini F., Wolf B., Flohe L.;
RT "Phospholipid hydroperoxide glutathione peroxidase is a selenoenzyme
RT distinct from the classical glutathione peroxidase as evident from
RT free and amino acid sequencing.";
RL Euk. Radic. Res. Commun. 14:343-361(1991).
CC -1- FUNCTION: COULD PLAY A MAJOR ROLE IN PROTECTING MAMMALS FROM THE
CC TOXICITY OF INGESTED LIPID HYDROPEROXIDES.
CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized
CC glutathione + 2 H(2)O.
CC -1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS
CC ENCODED BY THE OPAL CODON, UGA.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Mitochondrial and cytoplasmic.
CC -1- ALTERNATIVE PRODUCTS: A SINGLE NUCLEAR GENE PRODUCES BOTH FORMS
CC BY USE OF ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
CC
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CC
CC EMBL: L12743; AAA31099.2; -;
CC EMBL: L12743; AAA31098.2; ALT_SEQ.
CC EMBL: X76009; CA53596.1; ALT_INIT.
CC EMBL: X76008; CA53595.1; ALT_INIT.
CC EMBL: S80257; AAB21327.2; -;
CC PIR: JN0608; JN0608.
CC HSP: P00435; 1GP1.
CC InterPro: IPR000889; Glut_peroxidase.
CC Pfam: PF00255; GSHpx.1.
CC PRINTS: PR01011; GLUTATHIONE_PEROXID_1; 1.
CC PROSITE: PS00460; GLUTATHIONE_PEROXID_2; 1.
CC OXidoreductase; Peroxidase; Selenium; Selenocysteine;
CC Mitochondrion; Transit peptide; Alternative initiation.
CC TRANSIT 1 7
CC CHAIN 2 197 MITOCHONDRION (POTENTIAL).
CC PHOSPHOLIPID HYDROPEROXIDE GLUTATHIONE
CC PEROXIDASE, MITOCHONDRIAL ISOFORM.
CC PHOSPHOLIPID HYDROPEROXIDE GLUTATHIONE
CC PEROXIDASE, CYTOPLASMIC ISOFORM.
CC INIT_MET 28 28
CC SECTS 73 73 FOR CYTOPLASMIC ISOFORM.

SQ SEQUENCE 197 AA; 22290 MW; 348645ABE35A7FD0 CRC64;
Query Match 30.8%; Score 303; DB 1; Length 197;
Best Local Similarity 40.18; Pred. No. 2.7e-22;
Matches 69; Conservative 29; Mismatches 60; Indels 14; Gaps 5;
QY 1 MVAATVAAAMLLMAACAQOE-----QDFYDEKAVIRKGLVLEKRGSLVYVAVS 55
DB 14 LIGCTTAVPGIA--GTMCASRDMDRCARSHHEFSANKIDDHNNLDKRYRCVIVAVS 71
QY 56 ECGFTDQHYRALQQLRDLPHEFNVAIFPCNPGQOEPDSNKEIESFACRTYSVSPMF 115
DB 72 QCGKTEVNYQQLVDLHARVAECGLRIAPFPCNPGFGRPEPSDAIEKEFAA-GYNVAFDMF 130
QY 116 SKIAVNTGTHAPAFKYL-AQTSCK-----EPYNNEMKYLVAAPGKYVGAMPD 161
DB 131 SKICVNGDDAHPIMKMKVOPKRGMLGNAIKMFETFLIDKNGCVVKRYRP 182
RESULT 14
BSAA_BACSU STANDARD; PRT; 160 AA.
ID BSAA_BACSU STANDARD; PRT; 160 AA.
AC P52035;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glutathione peroxidase homolog bsaa.
GN BSAA.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
CC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / MARBURG;
RX MEDLINE=96349105; PubMed=8760912;
RA Sorokin A.V., Azevedo V., Zumbstein E., Galleron N., Ehrlich S.D.,
RA Seror P.;
RT "Sequence analysis of the Bacillus subtilis chromosome region between
RT the sera and kgd loci cloned in a yeast artificial chromosome.";
RL Microbiology 142:2005-2016(1996).
CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
CC
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CC
CC EMBL: L77246; AAA96626.1; -;
CC EMBL: Z99115; CAB14108.1; -;
CC HSP: P00435; 1GP1.
CC Subtilisin; BG11530; bsaa.
CC InterPro: IPR000889; Glut_peroxidase.
CC Pfam: PF00255; GSHpx.1.
CC PRINTS: PR01011; GLUTATHIONE_PEROXID_1; 1.
CC PROSITE: PS00460; GLUTATHIONE_PEROXID_2; 1.
CC OXidoreductase; Peroxidase; Complete proteome.
CC ACT_SITE 35 35 BY SIMILARITY.
SQ SEQUENCE 160 AA; 18256 MW; 59821F065634E404 CRC64;
Query Match 30.2%; Score 297; DB 1; Length 160;
Best Local Similarity 38.6%; Pred. No. 8e-22;
Matches 61; Conservative 26; Mismatches 65; Indels 6; Gaps 2;
QY 26 YDKRAVIRKGLVLEKRGSLVYVAVSECGFTDQHYRALQQLRDLPHEFNVAAP 85
DB 4 YHMKVIRITGKDMTLPQFAKGLIMIVATSKCGFTSQ-LKQLOELVDYVQOEGELTIGFP 62

QY 86 CNOFGQOEEDSNKEIESFACRTYSVSFPMFSKIATVGTGAHPAFKYLQ-----TSQKEP 140
DB 63 CNOFMNQEPEGEADIDIEFCETINYGTFPMFSKIDVANGKNAHPLFVYLTEHAKMLGKTAT 122
QY 141 TNNFMKYLVAPODGKVVGAMPDPTVSVEEVRLOITATLVK 178
DB 123 KNNFTKFIYDRNGEIVGRYSPNTNPKLEDDIVKLEQ 160

RESULT 15

GSHT_YEAST
ID GSHT_YEAST STANDARD; PRT; 162 AA.
AC P38143;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Glutathione peroxidase homolog YBR244W (EC 1.11.1.9).
GN YBR244W OR YBR1632.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxId=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Aljinovic G., Pohl F.M., Pohl T.M.;
RL Submitted (Aug-1994) to the EMBL/Genbank/DBJ databases.
CC -1 FUNCTION: MAY CONSTITUTE A GLUTATHIONINE PEROXIDASE-LIKE
CC PROTECTIVE SYSTEM AGAINST OXIDATIVE STRESSES (BY SIMILARITY).
CC -1 CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) -> oxidized
CC glutathione + 2 H(2)O.
CC -1 SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
CC -----
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CC -----
DR EMBL; 236113; CAA85207.1; -
DR PIR; S46121; S46121.
DR HSSP; P00435; 1GPI.
DR SGD; S0000448; YBR244W.
DR InterPro: IPR000889; Glut_peroxidase.
DR Pfam: PF00255; GSHpx; 1.
DR PRINTS; PRO1011; GLUTPROXOASE.
DR PROSITE; PS00460; GLUTATHIONE_PEROXID_1; 1.
DR PROSITE; PS00763; GLUTATHIONE_PEROXID_2; 1.
KW Hypothetical protein; Oxidoreductase; Peroxidase.
FT ACT SITE 37 BY SIMILARITY.
SQ SEQUENCE 162 AA; 18406 MW; BD02E7E6D38527A6 CRC64;

Query Match 29.3%; Score 288; DB 1; Length 162;
Best Local Similarity 39.0%; Pred. No. 6e-21;
Matches 62; Conservative 31; Mismatches 60; Indels 6; Gaps 3;

QY 25 FYDFKAVNIRGKIVLSLEKRGVSLVNVNASCEGFTDQHRALQQLORDIGPHHENVLAP 84
DB 5 FYDLECKDKKESFQDKGVKVLIVNASCGFTPO-YKELEELYKKYQDKGFVILGP 63
QY 85 PCNOFGQOEEDSNKEIESFACRTYSVSFPMFSKIATVGTGAHPAFKYL-AQTSG----KE 139
DB 64 PCNOFGQOEEDSNKEIESFACRTYSVSFPMFSKIATVGTGAHPAFKYL-AQTSG----KE 139
QY 140 PTNNFMKYLVAPODGKVVGAMPDPTVSVEEVRLOITATLVK 178
DB 124 IKMNFKEFLVDSNGKVVGRFSSILTRPSLDOETQSILSK 162

Search completed: August 23, 2002, 14:39:57
Job time: 134 sec

Mon Aug 26 08:01:41 2002

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